

1	ACA	GTC	AGC	CGC	M	A	P	$\frac{L_{\text{GAA}}}{C_{\text{GAA}}} \cdot \frac{P_{\text{GAA}}}{P_{\text{GAA}}} \cdot \frac{S_{\text{GAA}}}{S_{\text{GAA}}} \cdot \frac{W_{\text{GAA}}}{W_{\text{GAA}}}$	L	P	L	1.2		
13	L	I	P	A	P	A	P	G	L	T	V	Q	2.8	
49	TTG	ATC	CCG	GCC	CCT	GCT	CCA	GGC	CTC	ACT	GTG	CAA	CTG	4.8
29	L	L	L	L	M	P	V	H	P	Q	R	L	S	9.6
97	CTG	CTG	CTG	CTG	ATG	CCT	GTC	CAT	CCC	CAG	AGG	TTG	CCC	4.4
45	E	D	S	P	L	G	G	G	S	S	E	D	P	14.4
145	GAG	GAT	TCC	CCC	TTG	GGA	GGA	GGC	TCT	TCT	GGG	GAA	GAT	19.2
61	G	E	E	D	L	P	S	E	E	D	S	P	L	6.0
193	GGC	GAG	GAG	GAT	CTG	CCC	AGT	GAA	GAG	GAT	TCA	CCC	AGA	24.0
77	P	P	G	E	E	D	L	P	G	E	D	L	P	7.6
241	CCA	CCC	GGG	GAG	GAG	GAT	CTA	CCT	GGA	GAG	GAT	CTA	CCT	24.0
93	E	D	L	P	E	V	K	P	K	S	E	E	G	9.2
289	GAG	GAT	CTA	CCT	GAA	GTT	AAG	CCT	AAA	TCA	GAA	GAG	GGC	28.8
109	K	L	E	D	L	P	T	V	E	A	P	G	D	10.8
337	AAG	TTA	GAG	GAT	CTA	CCT	ACT	GTT	GAG	GCT	CCT	GGA	GAT	3.36
125	P	Q	N	N	A	H	R	D	K	E	G	D	Q	1.40
385	CCC	CAG	AAT	AAT	GCC	CAC	AGG	GAC	AAA	GAA	GGG	GAT	GAC	4.32
141	W	R	Y	G	G	D	P	P	W	P	R	V	S	1.40
433	TGG	CGC	TAT	GGA	GGC	GAC	CCG	CCC	TGG	CCC	CGG	GTG	TCC	4.80
157	A	G	R	F	Q	S	P	V	D	I	R	P	Q	1.56
481	GCG	GGC	CGC	TTC	CAG	CGG	GTG	GAT	ATC	CGC	CCC	CAG	CTC	5.28

173	F	C	P	A	L	R	P	T	D	E	G	P	Q	L	P	188
529	TTC	TGC	CCG	GCC	CTG	CGC	CCC	CTG	GAA	CTC	CTG	GGC	TTC	CAG	CTC	CCG
577	CCG	CTC	CCA	GAA	CTG	CGC	CTG	CGC	AAC	AAT	GGC	CAC	AGT	GTG	CAA	CTG
205	T	L	P	P	G	L	E	M	A	L	G	P	G	R	E	Y
625	ACC	CTG	CCT	CCT	GGG	CTA	GAG	ATG	GCT	CTG	GGT	CCC	GGG	CAG	TAC	624
221	R	A	L	Q	L	H	L	H	W	G	A	A	G	R	P	G
673	CGG	GCT	CTG	CAG	CTG	CAT	CTG	CAC	TGG	GGG	GCT	GCA	GGT	CGT	CCG	GGC
237	S	E	H	T	V	E	G	H	R	F	P	A	E	I	H	V
721	TCG	GAG	CAC	ACT	GTG	GAA	GGC	CAC	CGT	TTC	CCT	GCC	GAG	ATC	CAC	GTG
253	V	H	L	S	T	A	F	A	R	V	D	E	A	L	G	R
769	GTT	CAC	CTC	AGC	ACC	GCC	TTT	GCC	AGA	GTT	GAC	GAG	GCC	TTG	GGG	CGC
269	P	G	G	L	A	V	L	A	A	F	L	E	E	G	P	E
817	CCG	GGG	GGC	CTG	GGC	GTG	TTG	GCC	GCC	TTT	CTG	GAG	GAG	GGC	CCG	GAA
285	E	N	S	A	Y	E	Q	L	L	S	R	L	E	E	I	A
865	GAA	AAC	AGT	GCC	TAT	GAG	CAG	TTG	CTG	TCT	CGC	TTG	GAA	GAA	ATC	GCT
301	E	E	G	S	E	T	Q	V	P	G	L	D	I	S	A	L
913	GAG	GAA	GGC	TCA	GAG	ACT	CAG	GTC	CCA	GGA	CTG	GAC	ATA	TCT	GCA	CTC
317	L	P	S	D	P	S	R	Y	F	Q	Y	E	G	S	L	T
961	CTG	CCC	TCT	GAC	TTC	AGC	CGC	TAC	TTC	CAA	TAT	GAG	GGG	TCT	CTG	ACT
333	T	P	P	C	A	Q	G	V	I	W	T	V	F	N	Q	T
1009	ACA	CCG	CCC	TGT	GCC	CAG	GGT	GTC	ATC	TGG	ACT	GTG	TTT	AAC	CAG	ACA

349 V M L S A K Q L<sub>1</sub> H<sub>2</sub> P<sub>3</sub> T<sub>4</sub> I<sub>5</sub> L<sub>6</sub> S<sub>7</sub> C<sub>8</sub> Y<sub>9</sub> D<sub>10</sub> T<sub>11</sub>  
 1057 GTG ATG CTG AGT GCT AAG CAG CTC CAC ACC CTC TCT GAC ACC CTG TGG  
 365 G P G D S R L Q L N F R A T Q P  
 1105 GGA CCT GGT GAC TCT CGT CAG CTG AAC TTC CGA GCG ACG CAG CCT  
 381 L N G R V I E A S F P A G V D S  
 1153 TTG AAT GGG CGA GTG ATT GAG GCC TCC TTC CCT GCT GGA GTG GAC AGC  
 397 S P R A A E P V Q L N S C L A A  
 1201 AGT CCT CGG GCT GCT GAG CCA GTC CAG CTG AAT TCC TGC CTG GCT GCT  
 413 G D I L A L V F G L L F A V T S  
 1249 GGT GAC ATC CTA GCC CTG GTT TTT GGC CTC CTT TTT GCT GTC ACC AGC  
 429 V A F L V Q M R R Q H R R G T K  
 1297 GTC GCG TTC CTT GTG CAG ATG AGA AGG CAG CAC AGA AGG GGA ACC AAA  
 444 G G V S Y R P A E V A E T G A \* 460  
 1345 GGG GGT GTG AGC TAC CGC CCA GCA GAG GTA GCC GAG ACT GGA GCC TAG  
 1393 AGG CTG GAT CTT GGA GAA TGT GAG AAG CCA GCC AGA GGC ATC TGA GGG  
 1440 GGA GCC GGT AAC TGT CCT GTC CTG CTC ATT ATG CCA CTT CCT TTT AAC  
 1488 TGC CAA GAA ATT TTT TAA AAT AAA TAT TTA TAA T  
 1489 TGC CAA GAA ATT TTT TAA AAT AAA TAT TTA TAA T

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1522 FIG.-1A  
 FIG.-1B  
 FIG.-1C  
**FIG.-1C**

**FIG.-1C**

1 gatccctgtt gactcgac cttacccca accctgtgc ctctgaaaca tgagctgt  
 61 ccactcaggg taaaatggat taaggccgt gcaagatgtg ctttgtaaaa cagatgttt  
 121 aaggcggcat gctcgtaaag agtcatacc aatccctaat ctcaagtaat cagggacaca  
 181 aadactgcgg aaggccgcgg ggtcctgtc citaggaaaaac cagagacctt tgttcaacttg  
 241 ttatctgtac ctccccca ctatccca tggaccctgtc aatccccc ctgtgagaaa  
 301 cacccaaaga ttatcaataaa aaaaaaaaaaa aatccaaaaa aaaaaaaaaaaaa  
 361 aaaaaaaaaa gacttaacggaa tagttatggta taaaatggta gctttatggta aaggcaagta  
 421 aatgatcata tccaaaccca gacggccatc atcacagtc aagtcttaactt gattgtatct  
 481 ctttatcatl gtcatctttt ggatctacta gatttagtcat catcctaaaa attctccccc  
 541 aagttctaat tacgtttccaa acatttaggg gtttacatggaa gcttgaacct actacccct  
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 1141 ctgactttcgatccaccccg ctttgcattt aatccatattt ttggatgtt  
 1201 ccgcacccgtt ccaattttt gatccatattt aatccatattt ttggatgtt  
 1261 ttatgttcatat ttctttttttaatccatattt ttggatgtt  
 1321 gatgtcatat gttttttttt ctttgcattt aatccatattt ttggatgtt  
 1381 catgttataat cttttttttt ctttgcattt aatccatattt ttggatgtt  
 1441 tcattttttttt taccacccgtt atccatattt aatccatattt ttggatgtt  
 1501 ttgtttttgtt aggggtatgtt tccatattt aatccatattt ttggatgtt  
 1561 tcttgatcc cttttttttt ctttgcattt aatccatattt ttggatgtt  
 1621 actatttttt ttaaggccaaa tatgttataat ctttgcattt aatccatattt ttggatgtt  
 1681 catatctgcataat tccatattt aatccatattt ttggatgtt  
 1741 gttttttttt tttttttttt tttttttttt tttttttttt  
 1801 tggaaatgtt tttttttttt tttttttttt tttttttttt  
 1861 gttttttttt tttttttttt tttttttttt tttttttttt  
 1921 ttccactttttttt gttttttttt tttttttttt tttttttttt

1981 ttgcattttc ctttcttactg tgttaaaaaa aagtatggac ttgtctcgag aggtaggcca  
 2041 ttcttaatca tgatctttaa agatcaataa tataatccct tcaggattt tgtctttatt  
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 2161 ttgtctggc gcagtggctc acacctgtaa tccccggactt ttgggtggcc aagggtggaa  
 2221 gatcaattt gcctacttctt atabatctt ctaaaggcaga attcacatctt ctccctca  
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 2341 ttgttttttgg tttttttttt tttttttttt tgctttttttt tgctctgtca  
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 3361 agctttggta tggggggaggg ggcacaggggg cagacaaaacc tggtagact tggcccatc  
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 3481 cagcttcgtt ttccaaatgca cgttacagcccg gtacacacccg tggctggggg cacccccacag  
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 3721 ACCCAACTGGG CGAGGAGGAT CTGGCCCAAGTG AAGAGGATTTC ACCCAAGAGAG GAGGATCCAC  
 3781 CCGGAGAGGA GGATCTACCT GGAGAGAAGG ATCTACCTGT AGGGAGGAT CTACTGTGAG  
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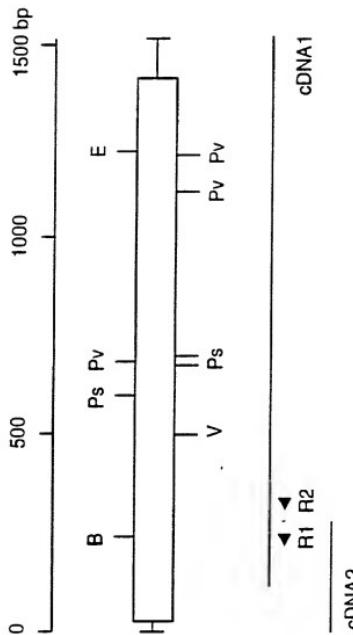
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 4261 aataatggtg tcagaggat tggggggaaa tgagggggaaa agtggggag  
 4321 gtggaaatgg taccaggac aaggaaagg aaggaaagg aaggaaagg aatggggatca ttttagggatca  
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 4441 actcccaagc caggaattttt gggaaagggg tggagacca tacaaggcg aggatgatgat  
 4501 ggggaaaga aagaagggg aaaggaaaga tgggtgtactc actcttttttgg gactaggac  
 4561 tgaatgtccc actcaatttt tttttttttt ttttttggac aaactttcac ttttttttggcc  
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 5461 CCTGGGCTTC CAGCTCCGGC CGCTCCAGA ACTGGGCCCTG CGCAAACATG GCCAACAGTGG  
 5521 tgggggggtc tccccggca gacttggggaa tgggggggggggg  
 5581 cgcatgtccct gccccgggggt tgggtggcc ttacccgggg  
 5641 cccatcgacg TGCAACTGAC CCTTGCCCTCT GGGCTAGAGA TGGCTCTGGGG  
 5701 GAGTACCGGG CTCTGCAAGCT GCATCTGAC TGGGGGGCTG CAGGTCTGGCC GGGCTCGGG  
 5761 CACATGTGG AAGGCCACCG TTTCCTGAC GAGgtgagcg cggactggcc  
 5821 aaaggagcg yggggacgggg ggccagagac tgggccctt cttaccctcg tgccttttgc  
 5881 agATCCACGT GGTTCACTTC AGCACCCGCT TTGGCCAGAT TGACGAGGGCC



7921 gactcttgtc tcaaaaaaaa aaaaaaaa gaaaaccaag caaaaaccaa aatgagacaa  
 7981 aaaaaacaag accaaaaaat ggttttggg aatttgtcaag gtcaagtctg gagagctaa  
 8041 ctttttctga gaactgtta tottaataa gcatcaataa ttttaactt gtaaatactt  
 8101 ttgttgaaaa tcgttctttt cttagtcaact cttgggtcat tttaaabtcc acttaactcta  
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 8221 gttttgtata ttcaatatta ttcaatatta ttcaatatta ttcaatatta ttcaatatta  
 8281 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt  
 8341 9ccaggctgc tc当地caactc ct当地accctgtt gatccaccag cctcgoocto ccaaagtgt  
 8401 9ggattcat tttctttt aatttgtctt gggcttaaac ttgtggccca gcactttatg  
 8461 atggtaacaca gagtttaagag tttttttttt tttttttttt tttttttttt tttttttttt  
 8521 ctcccaccc cttccaccc ccccttotcc cttccaccc cttccaccc cttccaccc  
 8581 caggccctctt ccaggctgtc c'aaaagccctg tactttttttt tggttaacg ttttatggg  
 8641 aggccctgc ctttagtgaag aatgggtctc agatgtgtgt taccttggct tctggaggt  
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 8761 tagatcttcctt tcacaggctc AGAACTCAG GTCCCCAGGAC TGACATCATTC TGCACTCCTG  
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 9301 attttttttt aaaaatggcc aatgggtctgg aatgggtctgg acctttttt tttttttttt  
 9361 ccggagggtc tgggttgtaa ctgggtctgg accctttttt tttttttttt  
 9421 ccactgactgt ccactgactt ccactgactt ccactgactt ccactgactt  
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 9601 tggctgggtt ccccccaaggcc aatgggtttt tttttttttt  
 9661 atgggtgtc acagccggcc tttttttttt tttttttttt  
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 9781 ccattcagcc ccagggtctgc tcaaggccgc ctgtgttttcc tttttttttt  
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**FIG.\_2F****FIG.\_2A****FIG.\_2B****FIG.\_2C****FIG.\_2D****FIG.\_2E****FIG.\_2F****FIG.\_2**



# 5' MN Genomic Region

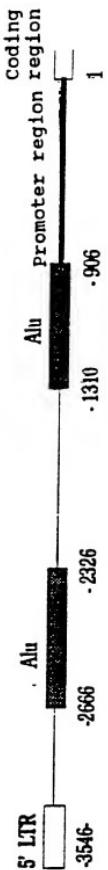


FIG.-4

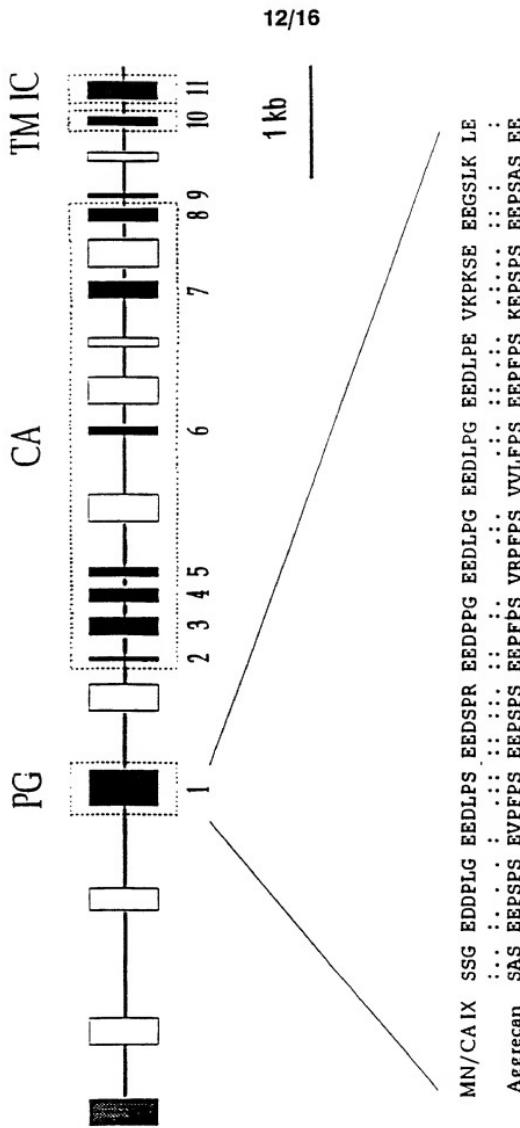


FIG.-5

T U C E G O : L C C / S E S G

-506	CTTGCTTTTC ATTCAAGCTC AAGTTGTCTT CCCACATACC CATTACTAA CTCACCCCTCG							
-446	<u>GGCTCCCTTA</u> GCA <u>GCTGCT</u> CT <u>ACCTCTTT</u> AC <u>CTGCCTCC</u> TGG <u>TGGACTC</u> AG <u>GGATGTAT</u> AP2							
-386	ACATGAGCTG CTTCCCTCT CAGCCAGAG ACATGGGGG CCCCAGCTCC CCTGCCTTTTC							
-326	CCCTTCGTG CCTGGAGCTG GGAAGCAGGC CAGGGTAGC TGAGGCTGGC TGGCAAGCAG							
-266	CTGGGTGGTG CCAGGGAGAG CCTGCATA <u>G</u> GCCAGGG <u>G</u> GT GCCTTGGTTT CCA <u>AGTAGT</u> VII p53							
-206	<u>CCATGGCCCC</u> GATAACCTTC TGCCTGTGCA CACACCTGCC CCT <u>CACTCCA</u> CCCC <u>CATCC</u> VI							
-146	AGCTTTGGTA TGGGGAGAG GG <u>ACAGGG</u> CAGACAAACC <u>TGTGAGACTT</u> TGG <u>CTCCATC</u> IV							
-86	<u>TCTGCAAAAG</u> GGG <u>GCTCTGT</u> GAG <u>TCAGCC</u> G <u>CTCCCCCTCC</u> AG <u>GGCTTGCTC</u> C <u>TCCCCCACC</u> II AP1 p53 I AP2 ***							
-26	CAGCTCTCGT TT <u>CCAATGCA</u> CGTA <u>CAGCCC</u> GTACACACCG TGTG <u>CTGGGA</u> CACCCCACAG ***							

*FIG.-6*

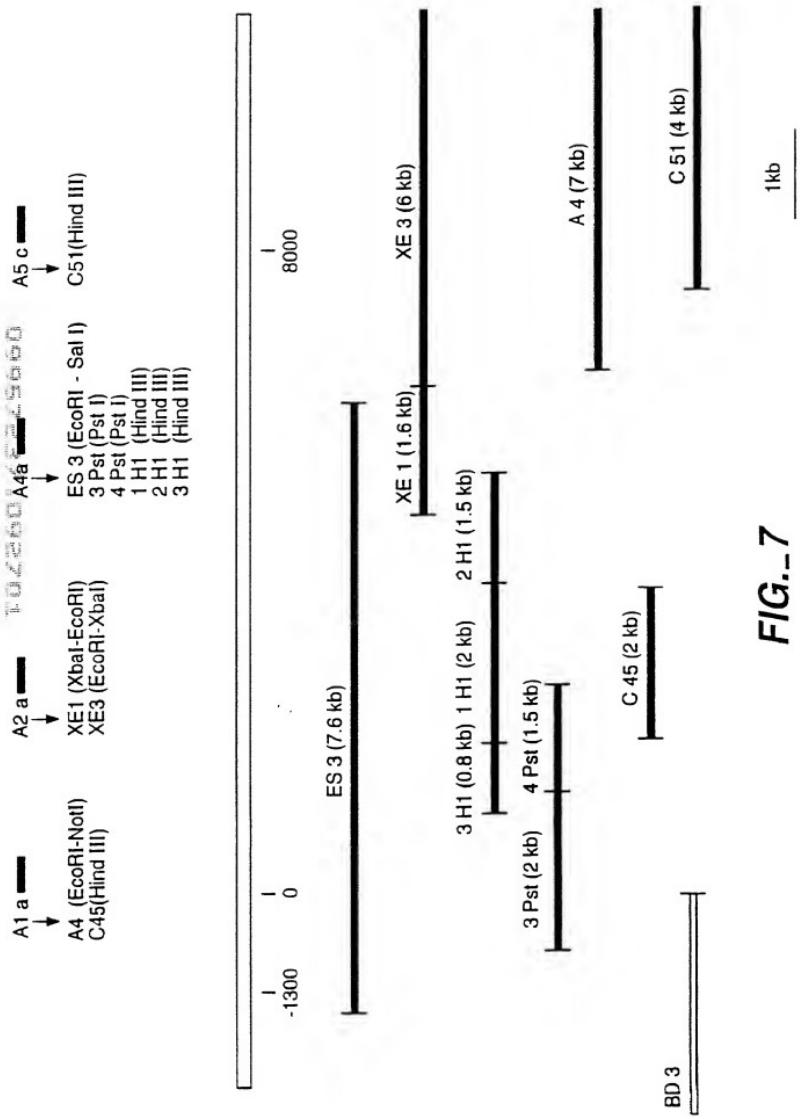


FIG.-7

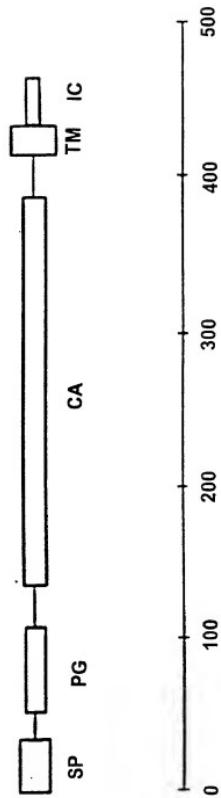
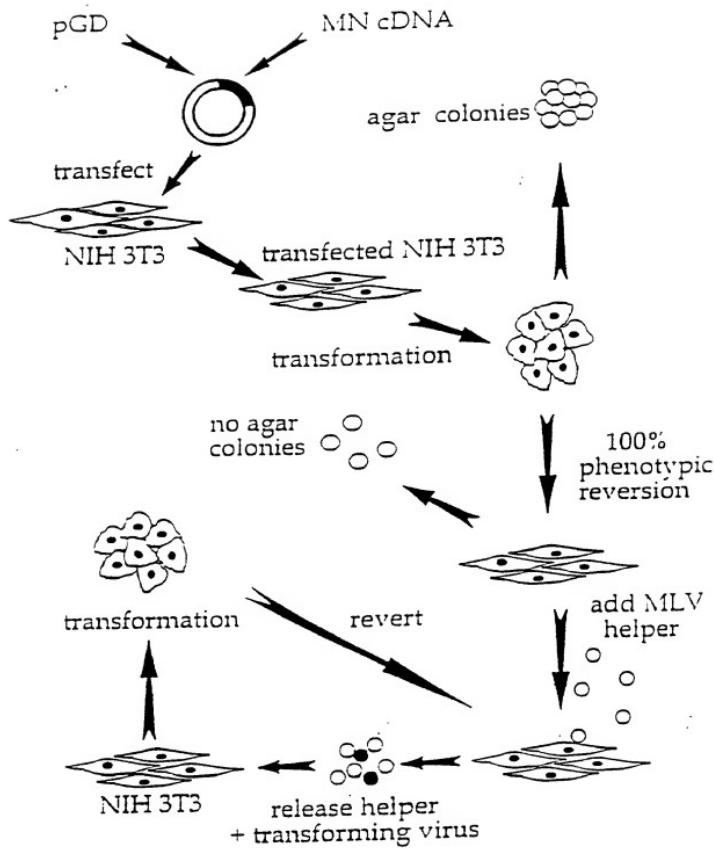


FIG.-8

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**FIG. 9**